POSTED 2/21/01

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| APPLICATION NO. | FILING DATE | FIRST NAMED INVENTOR | ATTORNEY DOCKET NO. |
|---|---|---|---|
| 09/479,877 | 01/10/00 | WOLF | M |

| EXAMINER | |
|---|---|
| PORTNER, V | |
| ART UNIT | PAPER NUMBER |
| 1645 | 5 |

DATE MAILED: 02/12/01

HM22/0212
ELIZABETH ARWINE PATENT ATTORNEY
U S ARMY MEDICAL RESEARCH & MATERIEL COM
504 SCOTT STREET
FORT DETRICK MD 21702-5021

**Please find below and/or attached an Office communication concerning this application or proceeding.**

**Commissioner of Patents and Trademarks**

USAMRMC
STAFF JUDGE ADVOCATE
FORT DETRICK, MD
2001 FEB 15 PM 3:13

PTO-90C (Rev. 2/95)

2 - Mail Copy

UNITED STATES DEPARTMENT OF COMMERCE
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Washington, D.C. 20231

| SERIAL NUMBER | FILING DATE | FIRST NAMED APPLICANT | ATTORNEY DOCKET NO. |
|---|---|---|---|
| 09/479,877 | 1/10/2000 | Wolf et al | |

| EXAMINER | |
|---|---|
| Portner | |
| ART UNIT | PAPER NUMBER |
| 1645 | 5 |
| DATE MAILED: | |

**Please find below a communication from the EXAMINER in charge of this application**

Commissioner of Patents

1. This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures.

2. Applicant is given ONE MONTH, or THIRTY DAYS, whichever is longer, from the mailing date of this letter within which to comply with the sequence rules, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136(a). In no case may an applicant extend the period for reply beyond the SIX MONTH statutory period. Direct the reply to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the reply.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Ginny Portner whose telephone number is (703)308-7543. The examiner can normally be reached on Monday through Friday from 7:30 AM to 5:00 PM except for the first friday of each two week period.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Lynette Smith, can be reached on (703) 308-3909. The fax phone number for this group is (703) 308-4242.

The Group and/or Art Unit location of your application in the PTO will be Group Art Unit 1645. To aid in correlating any papers for this application, all further correspondence regarding this application should be directed to this Art Unit.

Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 308-0196.

LRS

LYNETTE R. F. SMITH
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600

Application No.: 09/47 377

# NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☒ 7. Other: additional sequences found

## Applicant Must Provide:

☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
PatentIn Software Program Support (SIRA)
Technical Assistance.....703-287-0200
To Purchase PatentIn Software.....703-306-2600

**PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE**

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Wolf, Marcia K
Cassels, Fred J
Boedeker, Edgar C

(ii) TITLE OF INVENTION: Transformed Bacteria Producing GS6 Antigens as Vaccines

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Hendricks and Assoc
(B) STREET: P.O. Box 2509
(C) CITY: Fairfax
(D) STATE: VA
(E) COUNTRY: US
(F) ZIP: 22031

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 09/479,877
(B) FILING DATE: 10-JAN-2000
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Hendricks, Glenna M
(B) REGISTRATION NUMBER: 32,535

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 703/425-8405
(B) TELEFAX: 703/425-8406

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4875 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAGCTTGTAA CCAGTTGATA AAAATATATC ACGCTGGGAA TGACGTGATG TATATACGGA 60

GCAGCTATGT CGGAACAGAT ATTTTCCTAT CGGTATGCGT TGTGAGTAAG CGTAAAGCCA 120

ATGCTGTCTG TAACTCCTGA TCCTTGCAGA CTAAATTAGA GCTCCTTCTA AATTAGACGG 180

ATGGATAAAC CTACAGACTG GCGCTCTGGG TCTCGCCGGA TATTTTCTAA TGAATTTAAG 240

CTTCATATGG TTGAACTGGC TTCGAAACCA AATGCCAATG TCGCACAACT GGCTCGGGAA 300

CATGGCGTTG ATAACAACCT GATTTTTAAA TAGCTACGCC TCTGGCAAAG AGAAGGACGT 360

ATTTCTCGTA GAATGCCTCC AACTATTGTA GGCCCTACAG TACCACTGAG GTAGCCTGAA 420

TTTAAAGCCG AAGCGGTCAG AACTGTTCTT GGTGTGAACG TAGCACTCAC CAATAAAAGC 480

ATCAATACGG TGCTCTGTTG ACACATTACG AATGTTATGT ATACAATAAA AATGATTATA 540

GCAATATTAA TGGTGTTATA TGAAGAAAAC AATTGGTTTA ATTCTAATTC TTGCTTCATT 600

CGGCAGCCAT GCCAGAACAG AAATAGCGAC TAAAAACTTC CCAGTATCAA CGACTATTTC 660

AAAAAGTTTT TTTGCACCTG AACCACGAAT ACAGCCTTCT TTTGGTGAAA ATGTTGGAAA 720

GGAAGGAGCT TTATTATTTA GTGTGAACTT AACTGTTCCT GAAAATGTAT CCCAGGTAAC 780

GGTCTACCCT GTTTATGATG AAGATTATGG GTTAGGACGA CTAGTAAATA CCGCTGATGC 840

TTCCCAATCA ATAATCTACC AGATTGTTGA TGAGAAAGGG AAAAAAATGT TAAAAGATCA 900

TGGTGCAGAG GTTACACCTA ATCAACAAAT AACTTTTAAA GCGCTGAATT ATACTAGCGG 960

GGAAAAAAAA ATATCTCCTG GAATATATAA CGATCAGGTT ATGGTTGGTT ACTATGTAAA 1020

CTAAATACTG GAAGTATGAT TATGTTGAAA AAAATTATTT CGGCTATTGC ATTAATTGCA 1080

GGAACTTCCG GAGTGGTAAA TGCAGGAAAC TGGCAATATA AATCTCTGGA TGTAAATGTA 1140

AATATTGAGC AAAATTTTAT TCCAGATATT GATTCCGCTG TTCGTATAAT ACCTGTTAAT 1200

TACGATTCGG ACCCGAAACT GGATTCACAG TTATATACGG TTGAGATGAC GATCCCTGCA 1260

GGTGTAAGCG CAGTTAAAAT CGCACCAACA GATAGTCTGA CATCTTCTGG ACAGCAGATC 1320

GGAAAGCTGG TTAATGTAAA CAATCCAGAT CAAAATATGA ATTATTATAT CAGAAAGGAT 1380

TCTGGCGCTG GTAACTTTAT GGCAGGACAA AAAGGATCCT TTCCTGTCAA AGAGAATACG 1440

TCATACACAT TCTCAGCAAT TTATACTGGT GGCGAATACC CTAATAGCGG ATATTCGTCT 1500

GGTACTTATG CAGGAAATTT GACTGTATCA TTTTACAGCA ATTAAAAAAA GGCCGCATTA 1560

TTGCGGCCAT TGACGATACT GCTAGGCAAA AATATGAAAT CAAAGTTAAT TATACTATTG 1620

ACGTTAGTGC CATTTTCATC TTTTTCAACA GGAAATAATT TTGAAATAAA TAAGACACGA 1680

GTAATTTACT CTGACAGCAC ACCATCAGTT CAAATATCAA ATAATAAAGC ATATCCTTTA 1740

ATTATTCAAA GCAATGTATG GGATGAAAGC AATAATAAAA ATCATGACTT TATAGCAACA 1800

CCACCGATTT TTAAAATGGA AAGTGAAAGT CGGAATATAA TAAAAATAAT TAAAACAACT 1860

ATTAATTTGC CGGACTCTCA GGAAAGTATG AGATGGTTAT GTATTGAATC AATGCCACCA 1920

ATAGAAAAAA GTACTAAAAT AAACAGAAAA GAAGGAAGGA CAGACAGTAT TAATATCAGC 1980

ATTCGGGGGT GCATTAAACT GATATATCGA CCTGCCAGTG TTCCGTCTCC TGTTTTTAAT 2040

AATATAGTAG AAAAATTAAA ATGGCATAAA AATGGAAAGT ATCTTGTATT AAAAAATAAT 2100

ACACCCTATT ACATTAGCTT TTCTGAGGTT TTTTTTGATT CAGATAAAGT AAACAATGCA 2160

AAAGATATTT TATATGTAAA ACCATACTCA GAGAAGAAAA TAGATATCAG CAACAGAATA 2220

ATAAAAAAAA TCAAATGGGC TATGATTGAT GATGCTGGCG CAAAAACAAA ACTTTATGAA 2280

TCAATTTTAT AAAAAATCTC ATTACAGTAT ACAAAAACAT CAGATTACAG GCTTGCTTTT 2340

TTTGCTATTT ATATATCCTT TCTCAACCTC ATATGGAAAT GAACAATTTA GTTTTGACTC 2400

ACGATTCCTA CCATCAGGTT ATAATTACTC TTTAAATAGT AACTTACCTC CTGAAGGTGA 2460

GTATCTGGTT GATATTTATA TTAACAAAAT AAAAAAGGAG TCCGCGATTA TTCCTTTTTA 2520

TATAAAAGGA AATAAACTTG TACCATGTTT ATCAAAAGAA AAAATTTCAT CTTTGGGTAT 2580

CAACATTAAT AATAACGACA ACACAGAGTG TGTAGAAACA AGTAAGGCAG GTATTAGTAA 2640

TATCAGCTTT GAGTTTAGCT CTCTTCGTTT GTTTATTGCT GTACCGAAAA ATCTTCTGTC 2700

TGAGATTGAT AAAATATCAT CAAAGGATAT AGATAACGGG ATTCATGCTT TATTTTTTAA 2760

TTATCAAGTA AATACAAGGC TAGCCAATAA TAAAAATCGT TATGATTACA TTTCTGTTTC 2820

ACCAAATATA AATTATTTTT CATGGCGGTT GCGTAATCTT TTTGAATTTA ACCAAAACAA 2880

CGATGAAAAA ACATGGGAAA GAAACTACAC TTATCTAGAA AAAAGTTTTT ATGATAAAAA 2940

GCTAAACTTA GTCGTTGGTG AAAGTTATAC GAATTCAAAT GTTTATAATA ACTACTCTTT 3000

TACTGGTATT TCAGTTTCTA CAGATACAGA TATGTATACG CCAAGTGAAA TCGATTATAC 3060

ACCAGAAATT CATGGAGTGG CTGATTCAGA CTCTCAGATT ATTGTCAGGC AAGGCAACAC 3120

CATTATCATT AATGAAAGTG TTCCAGCCGG ACCGTTCTCA TTTCCAATAA CCAATCTCAT 3180

GTATACTGGG GGGCAACTTA ATGTGGAGAT AACAGATATT TATGGAAATA AAAAACAATA 3240

TACTGTCAAT AATTCCTCTC TTCCTGTTAT GAGAAAAGCG GGACTAATGG TATATAATTT 3300

TATATCTGGG AAATTAACAA AAAAAAATAG TGAGGATGGT GATTTTTTTA CTCAAGGTGA 3360

TATTAACTAC GGTACTCACT ATAACAGCAC ACTATTCGGT GGATATCAGT TTAGTAAAAA 3420

TTATTTTAAC TTATCTACTG GTATAGGCAC TGATCTGGGA TTTTCTGGAG CATGGCTACT 3480

ACACGTTAGC AGAAGTAATT TTAAGAATAA AAATGGATAT AATATTAATC TACAACAAAA 3540

CACTCAGTTA AGACCATTCA ATGCCGGGGT TAATTTCGAT TACGCATACA GAAAAAAAAG 3600

GTATGTGGAA CTTTCCGACA TTGGCTGGCA TGGTAATTTA TATAATCAAC TTAAAAATAG 3660

TTTTTCTTTA TCCTTGTCAA AATCATTGAA TAAATACGGA AATTTCTCAC TTGATTATAA 3720

CAAAATGAAA TACTGGGATA ATGCGTATGA TAGTAACTCA ATGTCGATTC GTTATTTTTT 3780

TAAATTCATG CGAGCAATGA TTACAACAAA TTGTTCTTTA AATAAATATC AATCTTATGA 3840

AAAAAAAGAT AAAAGATTTA GTATTAATAT ATCATTGCCT TTAACCAAAG ATTACGGGCA 3900

CATATCTTCA AACTATTCAT TTTCCAATGC AAATACAGGA ACGGCAACCA GTTCTGTAGG 3960

CTTAAACGGT AGTTTTTTTA ATGACGCAAG ATTAAACTGG AACATTCAGC AGAACAGAAC 4020

GACCCGTAAC AATGGATATA CTGATAATAC CAGTTACATA GCAACCAGCT ATGCCTCTCC 4080

CTATGGCGTT TTTACTGGTT CATATTCAGG ATCGAACAAG TATTCAAGCC AGTTTTATTC 4140

TGCATCGGGA GGTATTGTTT TGCATAGCGA TGGCGTAGCT TTTACTCAAA AAGCCGGAGA 4200

TACCTCTGCT CTTGTCCGTA TTGATAATAT TTCTGATATA AAAATTGGTA ACACTCCTGG 4260

TGTTTATACT GGGTATAATG GTTTTGCTTT AATTCCTCAT CTTCAGCCGT TCAAAAAAAA 4320

CACCATTTTA ATTAATGATA AAGGAATTCC AGACGGTATT ACTCTTGCTA ATATAAAAAA 4380

ACAAGTTATC CCATCACGAG GAGCTATTGT TAAAGTAAAA TTTGATGCTA AAAAAGGCAA 4440

TGACATTTTG TTTAAGCTTA CAACTAAAGA TGGAAAAACG CCCCCATTAG GAGCTATAGC 4500

CCATGAAAAA AATGGAAAAC AGATTAATAC GGGTATCGTT GACGATGATG GTATGCTTTA 4560

TATGTCTGGA TTATCAGGGA CAGGGATTAT TAATGTAACA TGGAATGGAA AAGTCTGTTC 4620

ATTTCCTTTT TCAGAAAAAG ATATATCTAG CAAACAATTA TCTGTTGTAA ATAAACAATG 4680

TTAGGTAGTG CATCCAATTA GTAGAACATG TGTTTTTCGA TAAACGCTCC GATCTCTTTT 4740

TCGTGGATCT CAACTGAGCG TGAGAAGCAG ATTGTTTTAC GAGCCAACCG CTTAATGCGG 4800

GTGCGTAGCG TCAGATTATT ACGCTCAATG CGTTGGGTGA ATATTTTGCC GGTCAGATGC 4860

TTATTCTTCG GTACC 4875

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGCCGCATTA TTGCGGCC 18

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGCCGCATTA TTGATTGCGG CC 22

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 527 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTGACACATT ACGAATGTTA TGTATACAAT AAAAATGATT ATAGCAATAT TAATGGTGTT 60

ATATGAAGAA AACAATTGGT TTAATTCTAA TTCTTGCTTC ATTCGGCAGC CATGCCAGAA 120

CAGAAATAGC GACTAAAAAC TTCCCAGTAT CAACGACTAT TTCAAAAAGT TTTTTTGCAC 180

CTGAACCACG AATACAGCCT TCTTTTGGTG AAAATGTTGG AAAGGAAGGA GCTTTATTAT 240

TTAGTGTGAA CTTAACTGTT CCTGAAAATG TATCCCAGGT AACGGTCTAC CCTGTTTATG 300

ATGAAGATTA TGGGTTAGGA CGACTAGTAA ATACCGCTGA TGCTTCCCAA TCAATAATCT 360

ACCAGATTGT TGATGAGAAA GGGAAAAAAA TGTTAAAAGA TCATGGTGCA GAGGTTACAC 420

CTAATCAACA AATAACTTTT AAAGCGCTGA ATTATACTAG CGGGGAAAAA AAAATATCTC 480

CTGGAATATA TAACGATCAG GTTATGGTTG GTTACTATGT AAACTAA 527

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 154 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Lys Lys Thr Ile Gly Leu Ile Leu Ile Leu Ala Ser Phe Gly Ser
1 5 10 15

His Ala Arg Thr Glu Ile Ala Thr Lys Asn Phe Pro Val Ser Thr Thr
20 25 30

Ile Ser Lys Ser Phe Phe Ala Pro Glu Pro Arg Ile Gln Pro Ser Phe
35 40 45

Gly Glu Asn Val Gly Lys Glu Gly Ala Leu Leu Phe Ser Val Asn Leu
50 55 60

Thr Val Pro Glu Asn Val Ser Gln Val Thr Val Tyr Pro Val Tyr Asp
65 70 75 80

Glu Asp Tyr Gly Leu Gly Arg Leu Val Asn Thr Ala Asp Ala Ser Gln
85 90 95

Ser Ile Ile Tyr Gln Ile Val Asp Glu Lys Gly Lys Lys Met Leu Lys
100 105 110

Asp His Gly Ala Glu Val Thr Pro Asn Gln Gln Ile Thr Phe Lys Ala
115 120 125

Leu Asn Tyr Thr Ser Gly Glu Lys Lys Ile Ser Pro Gly Ile Tyr Asn
130 135 140

Asp Gln Val Met Val Gly Tyr Tyr Val Asn
145 150

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 167 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Leu Lys Lys Ile Ile Ser Ala Ile Ala Leu Ile Ala Gly Thr Ser
1 5 10 15

Gly Val Val Asn Ala Gly Asn Trp Gln Tyr Lys Ser Leu Asp Val Asn
20 25 30

Val Asn Ile Glu Gln Asn Phe Ile Pro Asp Ile Asp Ser Ala Val Arg
35 40 45

Ile Ile Pro Val Asn Tyr Asp Ser Asp Pro Lys Leu Asp Ser Gln Leu
50 55 60

Tyr Thr Val Glu Met Thr Ile Pro Ala Gly Val Ser Ala Val Lys Ile
65 70 75 80

Ala Pro Thr Asp Ser Leu Thr Ser Ser Gly Gln Gln Ile Gly Lys Leu
85 90 95

Val Asn Val Asn Asn Pro Asp Gln Asn Met Asn Tyr Tyr Ile Arg Lys
100 105 110

Asp Ser Gly Ala Gly Asn Phe Met Ala Gly Gln Lys Gly Ser Phe Pro
115 120 125

Val Lys Glu Asn Thr Ser Tyr Thr Phe Ser Ala Ile Tyr Thr Gly Gly
130 135 140

Glu Tyr Pro Asn Ser Gly Tyr Ser Ser Gly Thr Tyr Ala Gly Asn Leu
145 150 155 160

Thr Val Ser Phe Tyr Ser Asn
165

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 212 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asn Asn Phe Glu Ile Asn Lys Thr Arg Val Ile Tyr Ser Asp Ser Thr
1 5 10 15

Pro Ser Val Gln Ile Ser Asn Asn Lys Ala Tyr Pro Leu Ile Ile Gln
20 25 30

Ser Asn Val Trp Asp Glu Ser Asn Asn Lys Asn His Asp Phe Ile Ala
35 40 45

Thr Pro Pro Ile Phe Lys Met Glu Ser Glu Ser Arg Asn Ile Ile Lys
50 55 60

Ile Ile Lys Thr Thr Ile Asn Leu Pro Asp Ser Gln Glu Ser Met Arg
65 70 75 80

Trp Leu Cys Ile Glu Ser Met Pro Pro Ile Glu Lys Ser Thr Lys Ile
85 90 95

Asn Arg Lys Glu Gly Arg Thr Asp Ser Ile Asn Ile Ser Ile Arg Gly
100 105 110

Cys Ile Lys Leu Ile Tyr Arg Pro Ala Ser Val Pro Ser Pro Val Phe
115 120 125

Asn Asn Ile Val Glu Lys Leu Lys Trp His Lys Asn Gly Lys Tyr Leu
130 135 140

Val Leu Lys Asn Asn Thr Pro Tyr Tyr Ile Ser Phe Ser Glu Val Phe
145 150 155 160

Phe Asp Ser Asp Lys Val Asn Asn Ala Lys Asp Ile Leu Tyr Val Lys
165 170 175

Pro Tyr Ser Glu Lys Lys Ile Asp Ile Ser Asn Arg Ile Ile Lys Lys
180 185 190

Ile Lys Trp Ala Met Ile Asp Asp Ala Gly Ala Lys Thr Lys Leu Tyr
195 200 205

Glu Ser Ile Leu
210

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 802 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Asn Gln Phe Tyr Lys Lys Ser His Tyr Ser Ile Gln Lys His Gln
1 5 10 15

Ile Thr Gly Leu Leu Phe Leu Leu Phe Ile Tyr Pro Phe Ser Thr Ser
20 25 30

Tyr Gly Asn Glu Gln Phe Ser Phe Asp Ser Arg Phe Leu Pro Ser Gly
35 40 45

Tyr Asn Tyr Ser Leu Asn Ser Asn Leu Pro Pro Glu Gly Glu Tyr Leu
50 55 60

Val Asp Ile Tyr Ile Asn Lys Ile Lys Lys Glu Ser Ala Ile Ile Pro
65 70 75 80

Phe Tyr Ile Lys Gly Asn Lys Leu Val Pro Cys Leu Ser Lys Glu Lys
85 90 95

Ile Ser Ser Leu Gly Ile Asn Ile Asn Asn Asn Asp Asn Thr Glu Cys
100 105 110

Val Glu Thr Ser Lys Ala Gly Ile Ser Asn Ile Ser Phe Glu Phe Ser
115 120 125

Ser Leu Arg Leu Phe Ile Ala Val Pro Lys Asn Leu Leu Ser Glu Ile
130 135 140

Asp Lys Ile Ser Ser Lys Asp Ile Asp Asn Gly Ile His Ala Leu Phe
145 150 155 160

Phe Asn Tyr Gln Val Asn Thr Arg Leu Ala Asn Asn Lys Asn Arg Tyr
165 170 175

Asp Tyr Ile Ser Val Ser Pro Asn Ile Asn Tyr Phe Ser Trp Arg Leu
180 185 190

Arg Asn Leu Phe Glu Phe Asn Gln Asn Asn Asp Glu Lys Thr Trp Glu
195 200 205

Arg Asn Tyr Thr Tyr Leu Glu Lys Ser Phe Tyr Asp Lys Lys Leu Asn
210 215 220

Leu Val Val Gly Glu Ser Tyr Thr Asn Ser Asn Val Tyr Asn Asn Tyr
225 230 235 240

Ser Phe Thr Gly Ile Ser Val Ser Thr Asp Thr Asp Met Tyr Thr Pro
245 250 255

Ser Glu Ile Asp Tyr Thr Pro Glu Ile His Gly Val Ala Asp Ser Asp
260 265 270

Ser Gln Ile Ile Val Arg Gln Gly Asn Thr Ile Ile Ile Asn Glu Ser
275 280 285

Val Pro Ala Gly Pro Phe Ser Phe Pro Ile Thr Asn Leu Met Tyr Thr
290 295 300

Gly Gly Gln Leu Asn Val Glu Ile Thr Asp Ile Tyr Gly Asn Lys Lys
305 310 315 320

Gln Tyr Thr Val Asn Asn Ser Ser Leu Pro Val Met Arg Lys Ala Gly
325 330 335

Leu Met Val Tyr Asn Phe Ile Ser Gly Lys Leu Thr Lys Lys Asn Ser
340 345 350

Glu Asp Gly Asp Phe Phe Thr Gln Gly Asp Ile Asn Tyr Gly Thr His
355 360 365

Tyr Asn Ser Thr Leu Phe Gly Gly Tyr Gln Phe Ser Lys Asn Tyr Phe
370 375 380

Asn Leu Ser Thr Gly Ile Gly Thr Asp Leu Gly Phe Ser Gly Ala Trp
385 390 395 400

Leu Leu His Val Ser Arg Ser Asn Phe Lys Asn Lys Asn Gly Tyr Asn
405 410 415

Ile Asn Leu Gln Gln Asn Thr Gln Leu Arg Pro Phe Asn Ala Gly Val
420 425 430

Asn Phe Asp Tyr Ala Tyr Arg Lys Lys Arg Tyr Val Glu Leu Ser Asp
435 440 445

Ile Gly Trp His Gly Asn Leu Tyr Asn Gln Leu Lys Asn Ser Phe Ser
450 455 460

Leu Ser Leu Ser Lys Ser Leu Asn Lys Tyr Gly Asn Phe Ser Leu Asp
465 470 475 480

Tyr Asn Lys Met Lys Tyr Trp Asp Asn Ala Tyr Asp Ser Asn Ser Met
485 490 495

Ser Ile Arg Tyr Phe Phe Lys Phe Met Arg Ala Met Ile Thr Thr Asn
500 505 510

Cys Ser Leu Asn Lys Tyr Gln Ser Tyr Glu Lys Lys Asp Lys Arg Phe
515 520 525

Ser Ile Asn Ile Ser Leu Pro Leu Thr Lys Asp Tyr Gly His Ile Ser
530 535 540

Ser Asn Tyr Ser Phe Ser Asn Ala Asn Thr Gly Thr Ala Thr Ser Ser
545 550 555 560

Val Gly Leu Asn Gly Ser Phe Phe Asn Asp Ala Arg Leu Asn Trp Asn
565 570 575

Ile Gln Gln Asn Arg Thr Thr Arg Asn Asn Gly Tyr Thr Asp Asn Thr
580 585 590

Ser Tyr Ile Ala Thr Ser Tyr Ala Ser Pro Tyr Gly Val Phe Thr Gly
595 600 605

Ser Tyr Ser Gly Ser Asn Lys Tyr Ser Ser Gln Phe Tyr Ser Ala Ser
610 615 620

Gly Gly Ile Val Leu His Ser Asp Gly Val Ala Phe Thr Gln Lys Ala
625 630 635 640

Gly Asp Thr Ser Ala Leu Val Arg Ile Asp Asn Ile Ser Asp Ile Lys
645 650 655

Ile Gly Asn Thr Pro Gly Val Tyr Thr Gly Tyr Asn Gly Phe Ala Leu
660 665 670

Ile Pro His Leu Gln Pro Phe Lys Lys Asn Thr Ile Leu Ile Asn Asp
675 680 685

Lys Gly Ile Pro Asp Gly Ile Thr Leu Ala Asn Ile Lys Lys Gln Val
690 695 700

Ile Pro Ser Arg Gly Ala Ile Val Lys Val Lys Phe Asp Ala Lys Lys
705 710 715 720

Gly Asn Asp Ile Leu Phe Lys Leu Thr Thr Lys Asp Gly Lys Thr Pro
725 730 735

Pro Leu Gly Ala Ile Ala His Glu Lys Asn Gly Lys Gln Ile Asn Thr
740 745 750

Gly Ile Val Asp Asp Asp Gly Met Leu Tyr Met Ser Gly Leu Ser Gly
755 760 765

Thr Gly Ile Ile Asn Val Thr Trp Asn Gly Lys Val Cys Ser Phe Pro
770 775 780

Phe Ser Glu Lys Asp Ile Ser Ser Lys Gln Leu Ser Val Val Asn Lys
785 790 795 800

Gln Cys

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 136 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Arg Thr Glu Ile Ala Thr Lys Asn Phe Pro Val Ser Thr Thr Ile Ser
1 5 10 15

Lys Ser Phe Phe Ala Pro Glu Pro Arg Ile Gln Pro Ser Phe Gly Glu
20 25 30

Asn Val Gly Lys Glu Gly Ala Leu Leu Phe Ser Val Asn Leu Thr Val
35 40 45

Pro Glu Asn Val Ser Gln Val Thr Val Tyr Pro Val Tyr Asp Glu Asp
50 55 60

Tyr Gly Leu Gly Arg Leu Val Asn Thr Ala Asp Ala Ser Gln Ser Ile
65 70 75 80

Ile Tyr Gln Ile Val Asp Glu Lys Gly Lys Lys Met Leu Lys Asp His
85 90 95

Gly Ala Glu Val Thr Pro Asn Gln Gln Ile Thr Phe Lys Ala Leu Asn
100 105 110

Tyr Thr Ser Gly Glu Lys Lys Ile Ser Pro Gly Ile Tyr Asn Asp Gln
115 120 125

Val Met Val Gly Tyr Tyr Val Asn
130 135

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly Asn Trp Gln Tyr Lys Ser Leu Asp Val Asn Val Asn Ile Glu Gln
1 5 10 15

Asn Phe Ile Pro Asp Ile Asp Ser Ala Val Arg Ile Ile Pro Val Asn
20 25 30

Tyr Asp Ser Asp Pro Lys Leu Asp Ser Gln Leu Tyr Thr Val Glu Met
35 40 45

Thr Ile Pro Ala Gly Val Ser Ala Val Lys Ile Ala Pro Thr Asp Ser
50 55 60

Leu Thr Ser Ser Gly Gln Gln Ile Gly Lys Leu Val Asn Val Asn Asn
65 70 75 80

Pro Asp Gln Asn Met Asn Tyr Tyr Ile Arg Lys Asp Ser Gly Ala Gly
85 90 95

Asn Phe Met Ala Gly Gln Lys Gly Ser Phe Pro Val Lys Glu Asn Thr
100 105 110

Ser Tyr Thr Phe Ser Ala Ile Tyr Thr Gly Gly Glu Tyr Pro Asn Ser
115 120 125

Gly Tyr Ser Ser Gly Thr Tyr Ala Gly Asn Leu Thr Val Ser Phe Tyr
130 135 140

Ser Asn
145